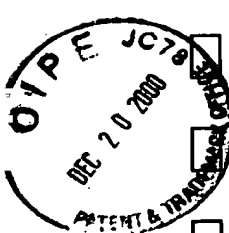


NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 
- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations.
 - ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
 - ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
 - ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
 - ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
 - ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
 - ☒ 7. Other: Both the paper copy and the computer readable form of the "Sequence Listing" fail to properly list the sequences depicted in Fig. 1C. The sequences purported to list these sequences, i.e. SEQ ID NOs: 7 and 8, do not find support in the specification as filed.

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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SEQUENCE LISTING

15/C
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<110> LONGACRE-ANDRE, SHIRLEY
ROTH, CHARLES
BARNWELL, JOHN
MENDIS, KAMINI
NATO, FARIDABANO

<120> RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
PLASMODIUM MSP-1

<130> 0660-0139-OXPCT

<140> 09/125,031

<141> 1999-03-10

<150> PCT/FR97/00290

<151> 1997-02-14

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<160> 15

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<211> 291

<212> DNA

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<222> (1)..(291)

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1				5				10					15			

aac	tct	ggc	tgt	ttc	aga	cac	ttg	gac	gag	aga	gag	gag	tgt	aaa	tgt	96
Asn	Ser	Gly	Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu	Cys	Lys	Cys	
		20					25					30				

ctg	ctg	aac	tac	aaa	cag	gag	ggc	gac	aag	tgc	gtg	gag	aac	ccc	aac	144
Leu	Leu	Asn	Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu	Asn	Pro	Asn	
		35					40					45				

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ccg acc tgt aac gag aac aac ggc ggc tgt gac gca gac gcc aaa tgc 192
Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys
    50                      55                      60

acc gag gag gac tcg ggc agc aac ggc aag aaa atc acg tgt gag tgt 240
Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys
    65                      70                      75                      80

acc aaa ccc gac tcg tac ccg ctg ttc gac ggc atc ttc tgc agc taa 288
Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser
          85                      90                      95

taa 291

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          20           25           30
Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn
          35           40           45
Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys
          50           55           60
Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys
          65           70           75           80
Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser
          85           90           95

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<210> 3
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<212> DNA
<213> Plasmodium falciparum

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tgtgttgaaa atccaaatcc tacttgtaac gaaaataatg gtggatgtga tgcagatgcc 180
aatgtaccg aagaagattc aggtagcaac ggaaagaaaa tcacatgtga atgtactaaa 240
cctgattcctt atccactttt cgatgggtatt ttctgcagt 279

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1 5 10 15

aac tct ggc tgt ttc aga cac ttg gac gag aga gag gag tgt aaa tgt 96
Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys
20 25 30

ctg ctg aac tac aaa cag gag ggc gac aag tgc gtg gag aac ccc aac 144
Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn
35 40 45

ccg acc tgt aac gag aac aac ggc ggc tgt gac gca gac gcc aaa tgc 192
Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys
50 55 60

acc gag gag gac tcg ggc agc aac ggc aag aaa atc acg tgt gag tgt 240
Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys
65 70 75 80

acc aaa ccc gac tcg tac ccg ctg ttc gac ggc atc ttc tgc agc tcc 288
Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser Ser
85 90 95

tct aac ttc ttg ggc atc tcg ttc ttg ttg atc ctc atg ttg atc ttg 336
Ser Asn Phe Leu Gly Ile Ser Phe Leu Leu Ile Leu Met Leu Ile Leu
100 105 110

tac agc ttc att taa taa 354
Tyr Ser Phe Ile
115

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Asn	Ser	Gly	Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu	Cys	Lys	Cys
		20						25					30		
Leu	Leu	Asn	Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu	Asn	Pro	Asn
		35					40					45			
Pro	Thr	Cys	Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala	Asp	Ala	Lys	Cys
	50					55					60				
Thr	Glu	Glu	Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile	Thr	Cys	Glu	Cys
65					70					75					80
Thr	Lys	Pro	Asp	Ser	Tyr	Pro	Leu	Phe	Asp	Gly	Ile	Phe	Cys	Ser	Ser
				85					90				95		
Ser	Asn	Phe	Leu	Gly	Ile	Ser	Phe	Leu	Leu	Ile	Leu	Met	Leu	Ile	Leu
			100					105					110		
Tyr	Ser	Phe	Ile												
			115												

<210> 6

<211> 342

<212> DNA

<213> Plasmodium falciparum

<400> 6

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tgtgttgaaa	atccaaatcc	tacttgtaac	gaaaataatg	gtggatgtga	tcagatgcc	180
aatgtaccg	aagaagattc	aggtagcaac	ggaaagaaaa	tcacatgtga	atgtactaaa	240
cctgattctt	atccactttt	cgatgggtatt	ttctgcagtt	cctctaactt	cttaggaata	300
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<210> 7

<211> 387

<212> DNA

<213> Plasmodium falciparum

<220>

<221> CDS

<222> (1)..(387)

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Met	Lys	Ala	Leu	Leu	Phe	Leu	Phe	Ser	Phe	Ile	Phe	Phe	Val	Thr	Lys	
1				5					10					15		
tgt	caa	tgt	gaa	aca	gaa	agt	tat	aag	cag	ctt	gta	gcc	aac	gtg	gac	96
Cys	Gln	Cys	Glu	Thr	Glu	Ser	Tyr	Lys	Gln	Leu	Val	Ala	Asn	Val	Asp	
			20					25					30			
gaa	ttc	aac	atc	tcg	cag	cac	caa	tgc	gtg	aaa	aaa	caa	tgt	ccc	gag	144
Glu	Phe	Asn	Ile	Ser	Gln	His	Gln	Cys	Val	Lys	Lys	Gln	Cys	Pro	Glu	
		35					40					45				
aac	tct	ggc	tgt	ttc	aga	cac	ttg	gac	gag	aga	gag	gag	tgt	aaa	tgt	192
Asn	Ser	Gly	Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu	Cys	Lys	Cys	
	50					55					60					
ctg	ctg	aac	tac	aaa	cag	gag	ggc	gac	aag	tgc	gtg	gag	aac	ccc	aac	240
Leu	Leu	Asn	Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu	Asn	Pro	Asn	
65					70				75					80		
ccg	acc	tgt	aac	gag	aac	aac	ggg	ggc	tgt	gac	gca	gac	gcc	aaa	tgc	288
Pro	Thr	Cys	Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala	Asp	Ala	Lys	Cys	
			85					90						95		
acc	gag	gag	gac	tcg	ggc	agc	aac	ggg	aag	aaa	atc	acg	tgt	gag	tgt	336
Thr	Glu	Glu	Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile	Thr	Cys	Glu	Cys	
			100					105					110			
acc	aaa	ccc	gac	tcg	tac	ccg	ctg	ttc	gac	ggc	atc	ttc	tgc	agc	taa	384
Thr	Lys	Pro	Asp	Ser	Tyr	Pro	Leu	Phe	Asp	Gly	Ile	Phe	Cys	Ser		
		115					120					125				
taa																387

<210> 8

<211> 127

<212> PRT

<213> Plasmodium falciparum

<400> 8

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Cys	Gln	Cys	Glu	Thr	Glu	Ser	Tyr	Lys	Gln	Leu	Val	Ala	Asn	Val	Asp	
			20					25					30			
Glu	Phe	Asn	Ile	Ser	Gln	His	Gln	Cys	Val	Lys	Lys	Gln	Cys	Pro	Glu	
		35					40					45				
Asn	Ser	Gly	Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu	Cys	Lys	Cys	
	50					55					60					

Leu	Leu	Asn	Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu	Asn	Pro	Asn
65					70					75					80
Pro	Thr	Cys	Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala	Asp	Ala	Lys	Cys
			85						90					95	
Thr	Glu	Glu	Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile	Thr	Cys	Glu	Cys
			100					105					110		
Thr	Lys	Pro	Asp	Ser	Tyr	Pro	Leu	Phe	Asp	Gly	Ile	Phe	Cys	Ser	
		115					120					125			

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<211> 330

<212> DNA

<213> Plasmodium falciparum

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<222> (1)..(330)

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1				5					10					15		

atc	tcg	cag	cac	caa	tgc	gtg	aaa	aaa	caa	tgt	ccc	gag	aac	tct	ggc	96
Ile	Ser	Gln	His	Gln	Cys	Val	Lys	Lys	Gln	Cys	Pro	Glu	Asn	Ser	Gly	
			20				25						30			

tgt	ttc	aga	cac	ttg	gac	gag	aga	gag	gag	tgt	aaa	tgt	ctg	ctg	aac	144
Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu	Cys	Lys	Cys	Leu	Leu	Asn	
		35					40					45				

tac	aaa	cag	gag	ggc	gac	aag	tgc	gtg	gag	aac	ccc	aac	ccg	acc	tgt	192
Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu	Asn	Pro	Asn	Pro	Thr	Cys	
	50					55					60					

aac	gag	aac	aac	ggc	ggc	tgt	gac	gca	gac	gcc	aaa	tgc	acc	gag	gag	240
Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala	Asp	Ala	Lys	Cys	Thr	Glu	Glu	
65				70						75					80	

gac	tcg	ggc	agc	aac	ggc	aag	aaa	atc	acg	tgt	gag	tgt	acc	aaa	ccc	288
Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile	Thr	Cys	Glu	Cys	Thr	Lys	Pro	
				85					90					95		

gac	tcg	tac	ccg	ctg	ttc	gac	ggc	atc	ttc	tgc	agc	taa	taa			330
Asp	Ser	Tyr	Pro	Leu	Phe	Asp	Gly	Ile	Phe	Cys	Ser					
			100					105					110			

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 <213> Plasmodium falciparum

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 20 25 30
 Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys Leu Leu Asn
 35 40 45
 Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn Pro Thr Cys
 50 55 60
 Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys Thr Glu Glu
 65 70 75 80
 Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys Thr Lys Pro
 85 90 95
 Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser
 100 105

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 <212> PRT
 <213> Plasmodium cynomolgi

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 20 25 30
 Ala Gly Met Tyr Lys Thr Ile Lys Lys Pro Leu Glu Asn His Val Asn
 35 40 45

Ala	Leu	Asn	Thr	Asn	Ile	Ile	Asp	Met	Leu	Asp	Ser	Arg	Leu	Lys	Lys	
	50					55					60					
Arg	Asn	Tyr	Phe	Leu	Asp	Val	Leu	Asn	Ser	Asp	Leu	Asn	Pro	Tyr	Ser	
	65				70					75					80	
Ile	Pro	His	Ser	Gly	Glu	Tyr	Ile	Ile	Lys	Asp	Pro	Tyr	Lys	Leu	Leu	
				85					90					95		
Asp	Leu	Glu	Lys	Lys	Lys	Leu	Leu	Gly	Ser	Tyr	Lys	Tyr	Ile	Gly	Ala	
			100					105						110		
Ser	Val	Asp	Lys	Asp	Met	Val	Thr	Ala	Asn	Asp	Gly	Leu	Ala	Tyr	Tyr	
		115					120					125				
Gln	Lys	Met	Gly	Asp	Leu	Tyr	Lys	Lys	His	Leu	Asp	Glu	Val	Asn	Ala	
	130					135					140					
Cys	Ile	Lys	Glu	Val	Glu	Ala	Asn	Ile	Asn	Lys	His	Asp	Glu	Glu	Ile	
	145				150					155					160	
Lys	Lys	Ile	Gly	Ser	Glu	Ala	Ser	Lys	Ala	Asn	Asp	Lys	Asn	Gln	Leu	
				165					170					175		
Asn	Ala	Lys	Lys	Glu	Glu	Leu	Gln	Lys	Tyr	Leu	Pro	Phe	Leu	Ser	Ser	
			180					185					190			
Ile	Gln	Lys	Glu	Tyr	Ser	Thr	Leu	Val	Asn	Lys	Val	His	Ser	Tyr	Thr	
		195					200					205				
Asp	Thr	Leu	Lys	Lys	Ile	Ile	Asn	Asn	Cys	Gln	Ile	Glu	Lys	Lys	Glu	
	210					215					220					
Thr	Glu	Thr	Ile	Val	Asn	Lys	Leu	Glu	Asp	Tyr	Ser	Lys	Met	Asp	Glu	
	225				230				235						240	
Glu	Leu	Asp	Val	Tyr	Lys	Gln	Ser	Lys	Lys	Glu	Asp	Asp	Val	Lys	Ser	
				245					250					255		
Ser	Gly	Leu	Leu	Glu	Lys	Leu	Met	Asn	Ser	Lys	Leu	Ile	Asn	Gln	Glu	
			260					265					270			
Glu	Ser	Lys	Lys	Ala	Leu	Ser	Glu	Leu	Leu	Asn	Val	Gln	Thr	Gln	Met	
		275					280					285				
Leu	Asn	Met	Ser	Ser	Glu	His	Arg	Cys	Ile	Asp	Thr	Asn	Val	Pro	Glu	
	290					295					300					
Asn	Ala	Ala	Cys	Tyr	Arg	Tyr	Leu	Asp	Gly	Thr	Glu	Glu	Trp	Arg	Cys	

305		310		315		320									
Leu	Leu	Tyr	Phe	Lys	Glu	Asp	Ala	Gly	Lys	Cys	Val	Pro	Ala	Pro	Asn
				325					330					335	
Met	Thr	Cys	Lys	Asp	Lys	Asn	Gly	Gly	Cys	Ala	Pro	Glu	Ala	Glu	Cys
			340					345					350		
Lys	Met	Asn	Asp	Lys	Asn	Glu	Ile	Val	Cys	Lys	Cys	Thr	Lys	Glu	Gly
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35 40 45
Ala Phe Asn Thr Asn Ile Thr Asp Met Leu Asp Ser Arg Leu Lys Lys
50 55 60
Arg Asn Tyr Phe Leu Glu Val Leu Asn Ser Asp Leu Asn Pro Phe Lys
65 70 75 80
Tyr Ser Pro Ser Gly Glu Tyr Ile Ile Lys Asp Pro Tyr Lys Leu Leu

85

90

95

Asp	Leu	Glu	Lys	Lys	Lys	Lys	Leu	Leu	Gly	Ser	Tyr	Lys	Tyr	Ile	Gly
			100					105					110		
Ala	Ser	Ile	Asp	Lys	Asp	Leu	Ala	Thr	Ala	Asn	Asp	Gly	Val	Thr	Tyr
		115					120					125			
Tyr	Asn	Lys	Met	Gly	Glu	Leu	Tyr	Lys	Thr	His	Leu	Thr	Ala	Val	Asn
	130					135					140				
Glu	Glu	Val	Lys	Lys	Val	Glu	Ala	Asp	Ile	Lys	Ala	Glu	Asp	Asp	Lys
145					150					155					160
Ile	Lys	Lys	Ile	Gly	Ser	Asp	Ser	Thr	Lys	Thr	Thr	Glu	Lys	Thr	Gln
				165					170					175	
Ser	Met	Ala	Lys	Lys	Ala	Glu	Leu	Glu	Lys	Tyr	Leu	Pro	Phe	Leu	Asn
			180					185					190		
Ser	Leu	Gln	Lys	Glu	Tyr	Glu	Ser	Leu	Val	Ser	Lys	Val	Asn	Thr	Tyr
		195					200					205			
Thr	Asp	Asn	Leu	Lys	Lys	Val	Ile	Asn	Asn	Cys	Gln	Leu	Glu	Lys	Lys
	210					215					220				
Glu	Ala	Glu	Ile	Thr	Val	Lys	Lys	Leu	Gln	Asp	Tyr	Asn	Lys	Met	Asp
225					230					235					240
Glu	Lys	Leu	Glu	Glu	Tyr	Lys	Lys	Ser	Glu	Lys	Lys	Asn	Glu	Val	Lys
				245					250					255	
Ser	Ser	Gly	Leu	Leu	Glu	Lys	Leu	Met	Lys	Ser	Lys	Leu	Ile	Lys	Glu
			260					265					270		
Asn	Glu	Ser	Lys	Glu	Ile	Leu	Ser	Gln	Leu	Leu	Asn	Val	Gln	Thr	Gln
		275					280					285			
Leu	Leu	Thr	Met	Ser	Ser	Glu	His	Thr	Cys	Ile	Asp	Thr	Asn	Val	Pro
	290					295					300				
Asp	Asn	Ala	Ala	Cys	Tyr	Arg	Tyr	Leu	Asp	Gly	Thr	Glu	Glu	Trp	Arg
305					310					315					320
Cys	Leu	Leu	Thr	Phe	Lys	Glu	Glu	Gly	Gly	Lys	Cys	Val	Pro	Ala	Ser
				325					330					335	
Asn	Val	Thr	Cys	Lys	Asp	Asn	Asn	Gly	Gly	Cys	Ala	Pro	Glu	Ala	Glu
			340					345					350		

Cys Lys Met Thr Asp Ser Asn Lys Ile Val Cys Lys Cys Thr Lys Glu
 355 360 365

Gly Ser Glu Pro Leu Phe Glu Gly Val Phe Cys Ser
 370 375 380

<210> 13

<211> 380

<212> PRT

<213> Plasmodium vivax-like sp.

<220>

<223> Amino Acids 1-140-REGION I

<220>

<223> Amino Acids 141-178-REGION II

<220>

<223> Amino Acids 179-283-REGION III

<220>

<223> Amino Acids 284-380-REGION IV

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Asp Gln Val Thr Thr Gly Glu Ala Glu Ser Glu Ala Pro Glu Ile Leu
 1 5 10 15

Val Pro Ala Gly Ile Ser Asp Tyr Asp Val Val Tyr Leu Lys Pro Leu
 20 25 30

Ala Gly Met Tyr Lys Thr Ile Lys Lys Gln Leu Glu Asn His Val Asn
 35 40 45

Ala Phe Asn Thr Asn Ile Thr Asp Met Leu Asp Ser Arg Leu Lys Lys
 50 55 60

Arg Asn Tyr Phe Leu Glu Val Leu Asn Ser Asp Leu Asn Pro Phe Lys
 65 70 75 80

Tyr Ser Ser Ser Gly Glu Tyr Ile Ile Lys Asp Pro Tyr Lys Leu Leu
 85 90 95

Asp Leu Glu Lys Lys Lys Lys Leu Ile Gly Ser Tyr Lys Tyr Ile Gly
 100 105 110

Ala Ser Ile Asp Met Asp Leu Ala Thr Ala Asn Asp Gly Val Thr Tyr
 115 120 125

Tyr	Asn	Lys	Met	Gly	Glu	Leu	Tyr	Lys	Thr	His	Leu	Asp	Gly	Val	Lys
130						135					140				
Thr	Glu	Ile	Lys	Lys	Val	Glu	Asp	Asp	Ile	Lys	Lys	Gln	Asp	Glu	Glu
145					150					155					160
Leu	Lys	Lys	Leu	Gly	Asn	Val	Asn	Ser	Gln	Asp	Ser	Lys	Lys	Asn	Glu
				165					170					175	
Phe	Ile	Ala	Lys	Lys	Ala	Glu	Leu	Glu	Lys	Tyr	Leu	Pro	Phe	Leu	Asn
			180					185					190		
Ser	Leu	Gln	Lys	Glu	Tyr	Glu	Ser	Leu	Val	Ser	Lys	Val	Asn	Thr	Tyr
		195					200					205			
Thr	Asp	Asn	Leu	Lys	Lys	Val	Ile	Asn	Asn	Cys	Gln	Leu	Glu	Lys	Lys
	210					215					220				
Glu	Ala	Glu	Ile	Thr	Val	Lys	Lys	Leu	Gln	Asp	Tyr	Asn	Lys	Met	Asp
225					230					235					240
Glu	Lys	Leu	Glu	Glu	Tyr	Lys	Lys	Ser	Glu	Lys	Lys	Asn	Glu	Val	Lys
				245					250					255	
Ser	Ser	Gly	Leu	Leu	Glu	Lys	Leu	Met	Lys	Ser	Lys	Leu	Ile	Lys	Glu
			260					265					270		
Asn	Glu	Ser	Lys	Glu	Ile	Leu	Ser	Gln	Leu	Leu	Asn	Val	Gln	Thr	Gln
		275					280					285			
Leu	Leu	Thr	Met	Ser	Ser	Glu	His	Thr	Cys	Ile	Asp	Thr	Asn	Val	Pro
	290					295					300				
Asp	Asn	Ala	Ala	Cys	Tyr	Arg	Tyr	Leu	Asp	Gly	Thr	Glu	Glu	Trp	Arg
305					310					315					320
Cys	Leu	Leu	Thr	Phe	Lys	Glu	Glu	Gly	Gly	Lys	Cys	Val	Pro	Ala	Ser
				325					330					335	
Asn	Val	Thr	Cys	Lys	Asp	Asn	Asn	Gly	Gly	Cys	Ala	Pro	Glu	Ala	Glu
			340					345					350		
Cys	Lys	Met	Thr	Asp	Ser	Asn	Lys	Ile	Val	Cys	Lys	Cys	Thr	Lys	Glu
		355					360					365			
Gly	Ser	Glu	Pro	Leu	Phe	Glu	Gly	Val	Phe	Cys	Ser				
	370					375					380				

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 <211> 281
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ALIGNMENT

<220>
 <223> Amino Acids 1-115-REGION I

<220>
 <223> Amino Acids 116-125-REGION II

<220>
 <223> Amino Acids 126-197-REGION III

<220>
 <223> Amino Acids 198-281-REGION IV

<400> 14

Asp	Gln	Val	Thr	Thr	Gly	Glu	Ala	Glu	Ser	Glu	Ala	Pro	Glu	Ile	Val
1				5					10					15	

Pro	Gly	Ile	Tyr	Asp	Val	Val	Tyr	Lys	Pro	Leu	Ala	Gly	Met	Tyr	Lys
			20					25					30		

Thr	Ile	Lys	Lys	Leu	Glu	Asn	His	Val	Asn	Ala	Asn	Thr	Asn	Ile	Asp
		35					40					45			

Met	Leu	Asp	Ser	Ala	Leu	Lys	Lys	Ala	Asn	Tyr	Phe	Leu	Val	Leu	Asn
	50					55					60				

Ser	Asp	Leu	Asn	Pro	Ser	Gly	Glu	Tyr	Ile	Ile	Lys	Asp	Pro	Tyr	Lys
65					70					75					80

Leu	Leu	Asp	Leu	Glu	Lys	Lys	Lys	Leu	Gly	Ser	Tyr	Lys	Tyr	Ile	Gly
				85					90					95	

Ala	Ser	Asp	Asp	Thr	Ala	Asn	Asp	Gly	Tyr	Tyr	Lys	Met	Gly	Leu	Tyr
			100					105					110		

Lys	His	Leu	Val	Lys	Val	Glu	Ile	Asp	Lys	Lys	Gly	Lys	Ala	Lys	Lys
		115					120					125			

Glu	Leu	Lys	Tyr	Leu	Pro	Phe	Leu	Ser	Gln	Lys	Glu	Tyr	Leu	Val	Lys
	130					135					140				

Val	Tyr	Thr	Asp	Leu	Lys	Lys	Ile	Asn	Asn	Cys	Gln	Glu	Lys	Lys	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145		150		155		160
Glu Val Lys Leu Asp Tyr Lys Met Asp Glu Leu Tyr Lys Ser Lys Val						
	165			170		175
Lys Ser Ser Gly Leu Leu Glu Lys Leu Met Ser Lys Leu Ile Glu Ser						
	180			185		190
Lys Leu Ser Leu Leu Asn Val Gln Thr Gln Leu Met Ser Ser Glu His						
	195			200		205
Cys Ile Asp Thr Asn Val Pro Asn Ala Ala Cys Tyr Arg Tyr Leu Asp						
	210			215		220
Gly Thr Glu Glu Trp Arg Cys Leu Leu Phe Lys Glu Gly Lys Cys Val						
	225			230		235
Pro Ala Asn Thr Cys Lys Asp Asn Gly Gly Cys Ala Pro Glu Ala Glu						
	245			250		255
Cys Lys Met Asp Asn Ile Val Cys Lys Cys Thr Lys Glu Gly Ser Glu						
	260			265		270
Pro Leu Phe Glu Gly Val Phe Cys Ser						
	275			280		

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<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:peptide

<400> 15

Leu Asn Val Gln Thr Gln

1

5